SEQUENCE LISTING

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Liu, Tao
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Wiberg, Eva

<120> USE OF GENES FOR INCREASING THE OIL CONTENT IN PLANTS

<130> 12810-00153-US

<150> PCT/EP2004/003845
<151> 2004-04-13

<150> EP 03008909.8
<151> 2003-04-16

<160> 43

<170> PatentIn version 3.3

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Tyr Pro Arg Arg Ser Pro Leu Trp Arg Phe Leu Ser Tyr Ser Thr Ser
             20                  25                  30

tta ctg acc ttc ggt gta tca aaa ctg ctt ctt ttc aca tgc tat aat   144
Leu Leu Thr Phe Gly Val Ser Lys Leu Leu Leu Phe Thr Cys Tyr Asn
         35                  40                  45

gtc aaa ttg aat ggt ttt gaa aaa tta gaa act gcc ttg gaa cgt tcc   192
Val Lys Leu Asn Gly Phe Glu Lys Leu Glu Thr Ala Leu Glu Arg Ser
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aaa agg gaa aat aga ggc ctt atg acg gtc atg aac cat atg agt atg   240
Lys Arg Glu Asn Arg Gly Leu Met Thr Val Met Asn His Met Ser Met
 65                  70                  75                  80
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gtc gat gat ccg tta gtt tgg gca aca cta cca tat aag tta ttt acg   288
Val Asp Asp Pro Leu Val Trp Ala Thr Leu Pro Tyr Lys Leu Phe Thr
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tct ttg gac aac ata aga tgg tct ttg ggt gca cat aat att tgc ttt   336
Ser Leu Asp Asn Ile Arg Trp Ser Leu Gly Ala His Asn Ile Cys Phe
            100                 105                 110

caa aat aaa ttt ctg gcc aac ttt ttc tca ctt ggc caa gtc ctt tca   384
Gln Asn Lys Phe Leu Ala Asn Phe Phe Ser Leu Gly Gln Val Leu Ser
        115                 120                 125

aca gaa aga ttt ggg gtg ggc cca ttt caa ggt tct ata gat gct tca   432
Thr Glu Arg Phe Gly Val Gly Pro Phe Gln Gly Ser Ile Asp Ala Ser
    130                 135                 140

ata aga ttg tta agc cct gac gac act tta gac ttg gaa tgg acc cct   480
Ile Arg Leu Leu Ser Pro Asp Asp Thr Leu Asp Leu Glu Trp Thr Pro
145                 150                 155                 160

cac tct gag gtc tct tct tcg cta aaa aaa gcc tac tcc ccg ccc ata   528
His Ser Glu Val Ser Ser Ser Leu Lys Lys Ala Tyr Ser Pro Pro Ile
                165                 170                 175

ata agg tcg aag cca tct tgg gtc cat gtt tat cca gaa gga ttt gta   576
Ile Arg Ser Lys Pro Ser Trp Val His Val Tyr Pro Glu Gly Phe Val
            180                 185                 190

cta caa tta tat ccg cct ttt gaa aat tcg atg agg tat ttt aaa tgg   624
Leu Gln Leu Tyr Pro Pro Phe Glu Asn Ser Met Arg Tyr Phe Lys Trp
        195                 200                 205

ggt att acc aga atg atc cta gaa gca aca aag ccg ccc att gta gta   672
Gly Ile Thr Arg Met Ile Leu Glu Ala Thr Lys Pro Pro Ile Val Val
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cca ata ttt gct aca ggg ttt gaa aaa ata gca tcc gaa gca gtc aca   720
Pro Ile Phe Ala Thr Gly Phe Glu Lys Ile Ala Ser Glu Ala Val Thr
225                 230                 235                 240

gat tca atg ttt aga caa att cta cca aga aac ttt ggc tct gaa ata   768
Asp Ser Met Phe Arg Gln Ile Leu Pro Arg Asn Phe Gly Ser Glu Ile
                245                 250                 255

aat gtt acc ata ggg gat cct tta aat gat gat tta atc gac agg tat   816
Asn Val Thr Ile Gly Asp Pro Leu Asn Asp Asp Leu Ile Asp Arg Tyr
            260                 265                 270

aga aaa gaa tgg aca cat ttg gtt gaa aaa tac tat gat ccc aaa aat   864
Arg Lys Glu Trp Thr His Leu Val Glu Lys Tyr Tyr Asp Pro Lys Asn
        275                 280                 285

cct aac gac ctc tct gac gaa ttg aaa tat ggt aaa gag gcg caa gat   912
Pro Asn Asp Leu Ser Asp Glu Leu Lys Tyr Gly Lys Glu Ala Gln Asp
    290                 295                 300

tta aga agc aga tta gcc gct gaa ctg aga gcc cat gtt gct gaa att   960
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Leu Arg Ser Arg Leu Ala Ala Glu Leu Arg Ala His Val Ala Glu Ile
305                 310                 315                 320

aga aat gaa gtt cgc aaa tta cca cgc gaa gac cct agg ttc aaa tcc   1008

Arg Asn Glu Val Arg Lys Leu Pro Arg Glu Asp Pro Arg Phe Lys Ser
                325                 330                 335

ccc tca tgg tgg aag cgg ttc aac acc acg gaa ggt aaa tcg gac cca   1056
Pro Ser Trp Trp Lys Arg Phe Asn Thr Thr Glu Gly Lys Ser Asp Pro
            340                 345                 350

gat gtt aaa gtc att ggc gaa aat tgg gca ata agg agg atg caa aag   1104
Asp Val Lys Val Ile Gly Glu Asn Trp Ala Ile Arg Arg Met Gln Lys
        355                 360                 365

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Leu Leu Thr Phe Gly Val Ser Lys Leu Leu Leu Phe Thr Cys Tyr Asn
         35                  40                  45
Val Lys Leu Asn Gly Phe Glu Lys Leu Glu Thr Ala Leu Glu Arg Ser
     50                  55                  60
Lys Arg Glu Asn Arg Gly Leu Met Thr Val Met Asn His Met Ser Met
 65                  70                  75                  80
Val Asp Asp Pro Leu Val Trp Ala Thr Leu Pro Tyr Lys Leu Phe Thr
                 85                  90                  95
Ser Leu Asp Asn Ile Arg Trp Ser Leu Gly Ala His Asn Ile Cys Phe
            100                 105                 110
Gln Asn Lys Phe Leu Ala Asn Phe Phe Ser Leu Gly Gln Val Leu Ser
        115                 120                 125
Thr Glu Arg Phe Gly Val Gly Pro Phe Gln Gly Ser Ile Asp Ala Ser
    130                 135                 140
Ile Arg Leu Leu Ser Pro Asp Asp Thr Leu Asp Leu Glu Trp Thr Pro
145                 150                 155                 160
His Ser Glu Val Ser Ser Ser Leu Lys Lys Ala Tyr Ser Pro Pro Ile
                165                 170                 175
Ile Arg Ser Lys Pro Ser Trp Val His Val Tyr Pro Glu Gly Phe Val
            180                 185                 190
Leu Gln Leu Tyr Pro Pro Phe Glu Asn Ser Met Arg Tyr Phe Lys Trp
        195                 200                 205

Gly Ile Thr Arg Met Ile Leu Glu Ala Thr Lys Pro Pro Ile Val Val
    210                 215                 220
Pro Ile Phe Ala Thr Gly Phe Glu Lys Ile Ala Ser Glu Ala Val Thr
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225                 230                 235                 240
Asp Ser Met Phe Arg Gln Ile Leu Pro Arg Asn Phe Gly Ser Glu Ile
                245                 250                 255
Asn Val Thr Ile Gly Asp Pro Leu Asn Asp Asp Leu Ile Asp Arg Tyr
            260                 265                 270
Arg Lys Glu Trp Thr His Leu Val Glu Lys Tyr Tyr Asp Pro Lys Asn
        275                 280                 285
Pro Asn Asp Leu Ser Asp Glu Leu Lys Tyr Gly Lys Glu Ala Gln Asp
    290                 295                 300
Leu Arg Ser Arg Leu Ala Ala Glu Leu Arg Ala His Val Ala Glu Ile
305                 310                 315                 320
Arg Asn Glu Val Arg Lys Leu Pro Arg Glu Asp Pro Arg Phe Lys Ser
                325                 330                 335
Pro Ser Trp Trp Lys Arg Phe Asn Thr Thr Glu Gly Lys Ser Asp Pro
            340                 345                 350
Asp Val Lys Val Ile Gly Glu Asn Trp Ala Ile Arg Arg Met Gln Lys
        355                 360                 365
Phe Leu Pro Pro Glu Gly Lys Pro Lys Gly Lys Asp Asp
    370                 375                 380
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ctg ttg ttc aat ctt aaa ctt cgt gat cga ttt cga atc gcc gtc gat   97
Leu Leu Phe Asn Leu Lys Leu Arg Asp Arg Phe Arg Ile Ala Val Asp
                  20                  25                  30

gat cac cgt ggt cga gct acg gtt ttc tca ccg gat ggt tgc ttc tct   145
Asp His Arg Gly Arg Ala Thr Val Phe Ser Pro Asp Gly Cys Phe Ser
              35                  40                  45

tcc act atc cac cgc tgg gtg act cga ttc cgg aac ttt cgc cgg gag   193
Ser Thr Ile His Arg Trp Val Thr Arg Phe Arg Asn Phe Arg Arg Glu
          50                  55                  60

tct ctc cct tct cca ccg gct ttt tat cgc aga cga gtt tct aag gac   241
Ser Leu Pro Ser Pro Pro Ala Phe Tyr Arg Arg Arg Val Ser Lys Asp
      65                  70                  75

tta acg gca gaa gaa gag tct gct ctt ttc cgg atg cta caa act gtg   289
Leu Thr Ala Glu Glu Glu Ser Ala Leu Phe Arg Met Leu Gln Thr Val
 80                  85                  90                  95

gct gtt ccc ctt att gga aat gct tgt cat gtt ttc atg aat ggt ttt   337
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Ala Val Pro Leu Ile Gly Asn Ala Cys His Val Phe Met Asn Gly Phe
                100                 105                 110

aac cgt gtt cag gta tat ggt tta gag aaa ttg cat gat gct tta ctc   385
Asn Arg Val Gln Val Tyr Gly Leu Glu Lys Leu His Asp Ala Leu Leu
            115                 120                 125

aac aga cca aag aac aag cct ctt gta acg gtg agc aat cat gtt gca   433
Asn Arg Pro Lys Asn Lys Pro Leu Val Thr Val Ser Asn His Val Ala
        130                 135                 140

tct gtg gat gat cca ttt gtc att gct tca tta ctt cca cct aaa ttt   481
Ser Val Asp Asp Pro Phe Val Ile Ala Ser Leu Leu Pro Pro Lys Phe
    145                 150                 155

cta ctt gat gcc cgt aat ttg agg tgg acg ctc tgt gct aca gat aga   529
Leu Leu Asp Ala Arg Asn Leu Arg Trp Thr Leu Cys Ala Thr Asp Arg
160                 165                 170                 175

tgc ttt aaa aac cct gta act tca gct ttc tct cga tct gtc aaa gtt   577
Cys Phe Lys Asn Pro Val Thr Ser Ala Phe Ser Arg Ser Val Lys Val
                180                 185                 190

ttg cca att tct cgt ggt gaa gga att tat cag cag gga atg gac att   625
Leu Pro Ile Ser Arg Gly Glu Gly Ile Tyr Gln Gln Gly Met Asp Ile
            195                 200                 205

gcg att tcg aaa ttg aac aac gga ggg tgg gtt cac atc ttt cca gaa   673
Ala Ile Ser Lys Leu Asn Asn Gly Gly Trp Val His Ile Phe Pro Glu
        210                 215                 220

ggc agt cgc tcc cgg gat ggt gga aag act atg ggc tca gcg aag agg   721
Gly Ser Arg Ser Arg Asp Gly Gly Lys Thr Met Gly Ser Ala Lys Arg
    225                 230                 235

ggt atc gga agg ttg att ttg gac gca gat act ctc cct atg gtt gtt   769
Gly Ile Gly Arg Leu Ile Leu Asp Ala Asp Thr Leu Pro Met Val Val
240                 245                 250                 255

cct ttt gtg cat act ggt atg cag gat ata atg cca gtt gga gct agt   817
Pro Phe Val His Thr Gly Met Gln Asp Ile Met Pro Val Gly Ala Ser
                260                 265                 270

gtt cca cgg att ggc aag aca gtg aca gtg atc att gga gac cct att   865
Val Pro Arg Ile Gly Lys Thr Val Thr Val Ile Ile Gly Asp Pro Ile
            275                 280                 285

cat ttt aat gac att ctc agc act gaa gga gcc caa cac gtc tca agg   913
His Phe Asn Asp Ile Leu Ser Thr Glu Gly Ala Gln His Val Ser Arg
        290                 295                 300

aaa cac ctg tat gac gcc gtt tcg tcc aga att gga caa aga ctg tac   961
Lys His Leu Tyr Asp Ala Val Ser Ser Arg Ile Gly Gln Arg Leu Tyr
    305                 310                 315

gat tta aaa gca caa gtt gat aga gta tat ata gaa caa caa tct atg   1009
Asp Leu Lys Ala Gln Val Asp Arg Val Tyr Ile Glu Gln Gln Ser Met
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320                 325                 330                 335

atg tca cac aat gcc aaa aca ccc tcg gac cgt gct gct gag atc ttt   1057
Met Ser His Asn Ala Lys Thr Pro Ser Asp Arg Ala Ala Glu Ile Phe
                340                 345                 350

cat aga gtc gat tgg gac tca ttt ggg atg gga gca caa ttt tca gaa   1105
His Arg Val Asp Trp Asp Ser Phe Gly Met Gly Ala Gln Phe Ser Glu
            355                 360                 365

gaa tca tca ccc agt agt aaa ccg att ggc caa agc gat gat cgc att   1153
Glu Ser Ser Pro Ser Ser Lys Pro Ile Gly Gln Ser Asp Asp Arg Ile
        370                 375                 380

gtc aga tct ccc aaa agg aga gtc tca ccc gaa gga ggg gtc agc ttg   1201
Val Arg Ser Pro Lys Arg Arg Val Ser Pro Glu Gly Gly Val Ser Leu
    385                 390                 395

aag att aag aag ctc atg gac tca acc gag atg atg ggg ttt gcg gct   1249
Lys Ile Lys Lys Leu Met Asp Ser Thr Glu Met Met Gly Phe Ala Ala
400                 405                 410                 415

aga ggg tta cta atg aac gag tac aag agt cgg gtt gaa tct gcc aat   1297
Arg Gly Leu Leu Met Asn Glu Tyr Lys Ser Arg Val Glu Ser Ala Asn
                420                 425                 430

gtt ggt agg cct tta aag gct tgg aga gag tat ttt atg aac cgt gga   1345
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Leu


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His Arg Gly Arg Ala Thr Val Phe Ser Pro Asp Gly Cys Phe Ser Ser
         35                  40                  45

Thr Ile His Arg Trp Val Thr Arg Phe Arg Asn Phe Arg Arg Glu Ser
     50                  55                  60

Leu Pro Ser Pro Pro Ala Phe Tyr Arg Arg Arg Val Ser Lys Asp Leu
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Thr Ala Glu Glu Glu Ser Ala Leu Phe Arg Met Leu Gln Thr Val Ala
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Val Pro Leu Ile Gly Asn Ala Cys His Val Phe Met Asn Gly Phe Asn
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Arg Val Gln Val Tyr Gly Leu Glu Lys Leu His Asp Ala Leu Leu Asn
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Arg Pro Lys Asn Lys Pro Leu Val Thr Val Ser Asn His Val Ala Ser
    130                 135                 140

Val Asp Asp Pro Phe Val Ile Ala Ser Leu Leu Pro Pro Lys Phe Leu
145                 150                 155                 160

Leu Asp Ala Arg Asn Leu Arg Trp Thr Leu Cys Ala Thr Asp Arg Cys
                165                 170                 175

Phe Lys Asn Pro Val Thr Ser Ala Phe Ser Arg Ser Val Lys Val Leu
            180                 185                 190

Pro Ile Ser Arg Gly Glu Gly Ile Tyr Gln Gln Gly Met Asp Ile Ala
        195                 200                 205

Ile Ser Lys Leu Asn Asn Gly Gly Trp Val His Ile Phe Pro Glu Gly
    210                 215                 220

Ser Arg Ser Arg Asp Gly Gly Lys Thr Met Gly Ser Ala Lys Arg Gly
225                 230                 235                 240

Ile Gly Arg Leu Ile Leu Asp Ala Asp Thr Leu Pro Met Val Val Pro
                245                 250                 255

Phe Val His Thr Gly Met Gln Asp Ile Met Pro Val Gly Ala Ser Val
            260                 265                 270

Pro Arg Ile Gly Lys Thr Val Thr Val Ile Ile Gly Asp Pro Ile His
        275                 280                 285

Phe Asn Asp Ile Leu Ser Thr Glu Gly Ala Gln His Val Ser Arg Lys
    290                 295                 300

His Leu Tyr Asp Ala Val Ser Ser Arg Ile Gly Gln Arg Leu Tyr Asp
305                 310                 315                 320

Leu Lys Ala Gln Val Asp Arg Val Tyr Ile Glu Gln Gln Ser Met Met
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Ser His Asn Ala Lys Thr Pro Ser Asp Arg Ala Ala Glu Ile Phe His
            340                 345                 350

Arg Val Asp Trp Asp Ser Phe Gly Met Gly Ala Gln Phe Ser Glu Glu
        355                 360                 365

Ser Ser Pro Ser Ser Lys Pro Ile Gly Gln Ser Asp Asp Arg Ile Val
    370                 375                 380

Arg Ser Pro Lys Arg Arg Val Ser Pro Glu Gly Gly Val Ser Leu Lys
385                 390                 395                 400
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Ile Lys Lys Leu Met Asp Ser Thr Glu Met Met Gly Phe Ala Ala Arg
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Gly Leu Leu Met Asn Glu Tyr Lys Ser Arg Val Glu Ser Ala Asn Val
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Trp Ala Ala Arg Ser Asp His Leu Gly Gly Ile Pro Arg Asn Thr Val
            10                  15                  20

ata atg gct gtt agt gca ttt gca aaa gca gta gca aat ctt tgc aat   151
Ile Met Ala Val Ser Ala Phe Ala Lys Ala Val Ala Asn Leu Cys Asn
        25                  30                  35

aaa agc tca gtt cac aat gca gat act ctt atg aat ctt gtc cag tca   199
Lys Ser Ser Val His Asn Ala Asp Thr Leu Met Asn Leu Val Gln Ser
    40                  45                  50

aga cca cct ggt gtt cct ctc atc act gtt agt aat cac atg tcg act   247
Arg Pro Pro Gly Val Pro Leu Ile Thr Val Ser Asn His Met Ser Thr
55                  60                  65                  70

ttg gat gat cca gta atg tgg ggg gca ttt aag ggt ctc ctt tcc tta   295
Leu Asp Asp Pro Val Met Trp Gly Ala Phe Lys Gly Leu Leu Ser Leu
                75                  80                  85

gat cca gaa ttg gct cgg tgg gtt ctt gct gca gag gat ata tgt ttc   343
Asp Pro Glu Leu Ala Arg Trp Val Leu Ala Ala Glu Asp Ile Cys Phe
            90                  95                  100

agg aac cct ata ttc tcc tac att ttc cgc act gga aaa tgt ata cct   391
Arg Asn Pro Ile Phe Ser Tyr Ile Phe Arg Thr Gly Lys Cys Ile Pro
        105                 110                 115

ata act aga ggt ggt gga atc tac caa gaa aac atg aat gaa gct ctc   439
Ile Thr Arg Gly Gly Gly Ile Tyr Gln Glu Asn Met Asn Glu Ala Leu
    120                 125                 130
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cag cga tta aaa gat gga tct tgg ctg cat acc ttc cca gag gga aag   487
Gln Arg Leu Lys Asp Gly Ser Trp Leu His Thr Phe Pro Glu Gly Lys
135                 140                 145                 150

gtg ttt caa gat gat gtt cct ata aga cga ctt aaa tgg gga act gca   535
Val Phe Gln Asp Asp Val Pro Ile Arg Arg Leu Lys Trp Gly Thr Ala
                155                 160                 165

agc ctc atc gcc cgt tcc cca gtt acc cca atc gtt ttg cca ata att   583
Ser Leu Ile Ala Arg Ser Pro Val Thr Pro Ile Val Leu Pro Ile Ile
            170                 175                 180

cac cgt ggt ttt gag gag atg atg ccg gag aac tac aat aat gga cga   631
His Arg Gly Phe Glu Glu Met Met Pro Glu Asn Tyr Asn Asn Gly Arg
        185                 190                 195

aga cca ctg gta ccg ttg ccg aac aaa cac ctt aaa gtt gtg gtt ggt   679
Arg Pro Leu Val Pro Leu Pro Asn Lys His Leu Lys Val Val Val Gly
    200                 205                 210

gaa cca att gag ttt gat gtt cca atg atg gtt gag act gct gtc ttg   727
Glu Pro Ile Glu Phe Asp Val Pro Met Met Val Glu Thr Ala Val Leu
215                 220                 225                 230

gac tcc cgc cat gta acc cct cct ctt caa gaa gtg aaa tgg cct gtc   775
Asp Ser Arg His Val Thr Pro Pro Leu Gln Glu Val Lys Trp Pro Val
                235                 240                 245

ctc act tct gct ggc caa gtg cta gac gaa act gct cag aga cac ctc   823
Leu Thr Ser Ala Gly Gln Val Leu Asp Glu Thr Ala Gln Arg His Leu
            250                 255                 260

tac ata gct ctg tcc gag aag att caa tcc tcc ttg gaa aca ttg aga   871
Tyr Ile Ala Leu Ser Glu Lys Ile Gln Ser Ser Leu Glu Thr Leu Arg
        265                 270                 275

ctc tta gcc aag cgg ttg tgacttccgc cgggaaactt catatcaaaa          919
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    280

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             20                  25                  30

Val Ala Asn Leu Cys Asn Lys Ser Ser Val His Asn Ala Asp Thr Leu
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         35                  40                  45

Met Asn Leu Val Gln Ser Arg Pro Pro Gly Val Pro Leu Ile Thr Val
     50                  55                  60

Ser Asn His Met Ser Thr Leu Asp Asp Pro Val Met Trp Gly Ala Phe
 65                  70                  75                  80

Lys Gly Leu Leu Ser Leu Asp Pro Glu Leu Ala Arg Trp Val Leu Ala
                 85                  90                  95

Ala Glu Asp Ile Cys Phe Arg Asn Pro Ile Phe Ser Tyr Ile Phe Arg
            100                 105                 110

Thr Gly Lys Cys Ile Pro Ile Thr Arg Gly Gly Gly Ile Tyr Gln Glu
        115                 120                 125

Asn Met Asn Glu Ala Leu Gln Arg Leu Lys Asp Gly Ser Trp Leu His
    130                 135                 140

Thr Phe Pro Glu Gly Lys Val Phe Gln Asp Asp Val Pro Ile Arg Arg
145                 150                 155                 160

Leu Lys Trp Gly Thr Ala Ser Leu Ile Ala Arg Ser Pro Val Thr Pro
                165                 170                 175

Ile Val Leu Pro Ile Ile His Arg Gly Phe Glu Glu Met Met Pro Glu
            180                 185                 190

Asn Tyr Asn Asn Gly Arg Arg Pro Leu Val Pro Leu Pro Asn Lys His
        195                 200                 205

Leu Lys Val Val Val Gly Glu Pro Ile Glu Phe Asp Val Pro Met Met
    210                 215                 220

Val Glu Thr Ala Val Leu Asp Ser Arg His Val Thr Pro Pro Leu Gln
225                 230                 235                 240

Glu Val Lys Trp Pro Val Leu Thr Ser Ala Gly Gln Val Leu Asp Glu
                245                 250                 255

Thr Ala Gln Arg His Leu Tyr Ile Ala Leu Ser Glu Lys Ile Gln Ser
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Ser Leu Glu Thr Leu Arg Leu Leu Ala Lys Arg Leu
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atgcttcaag aatgtagtca tgtcctacat gtttcgactt gggaaatgca taccaatcac 180
gagaggggt gggatttatc aagaacacat gaatgaagcc cttgacgtgc ttagaaatgg 240
aggctggctg catacattcc ctgaaggaaa aatagcccaa gaagatcagc cgattagaag 300
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<222> (423)..(423)
<223> n is a, c, g, or t

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ttcattgcct tcttccacct ctttctatcg taaacgagtg attaaggatt tcagttctga 180
ggaagattca gctcttgttc gtacgatgca agctgttgcg gttcctgttc ttggaaatgt 240
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ctccgcgttg ctgcatagac ctaagggcaa acctcttctt acggtcagca atcatgttgc 360
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tan 423

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tttttatcaa ccaacgcaac atgtcacgga cgatggagtg ggcggcgagg gcggagcacc 60
tccgcggcat tcccagaaaa ctcgtgattg cggcggtggg cggattcgcc aaaacggtgt 120
cgtctttcct caacaccgcc gatgttcaca acggcgacac tctcctccgc ctcgtccgct 180
ccagacccca ccgcgtcccc ctcattaccg ttagcaatca catgtccact ttggatgatc 240
cggttatgtg ggggttcaag ggttttccta tcttcgacac caacttagct cgctgggttc 300

tcgctgccga agatatttgc ttcaggaatg ccctctattc ctatattttt cggctgcata 360
cttttccaga aggaaaagtg tatcaagaag atgcacctat aaggcaat 408

<210> 10
<211> 368
<212> DNA
<213> Linum usitatissimum

<220>
<221> misc_feature
<222> (1)..(368)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 10
cggttagcaa ccatgttgct tctgtcgatg acccatttgt gattgcttca ttgctaccac 60
caagagtact tttggatgct cagaacttga ggtggacact ttgcgcaagg atcgctgttt 120
taggaatccc gtcacttctg cattcttaag actgtcaaag tcttgcccct ctctcgtggt 180
catggagttt atcagaaggg tatggacacg gcaattgcga acgtgaacac tggtggctgg 240
gttcacatct tcccggaggt agccgttcta aggatggtgg gaaaactatg gggtctatta 300
aaagaggtgt tggaaggttg gtacttgatg ctgatacttc tccccattgt agtcccggtc 360
gtgcacac 368

<210> 11
<211> 376
<212> DNA
<213> Linum usitatissimum

<220>
<221> misc_feature
<222> (1)..(376)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 11
tcgtagttag agaacctcag atggctggga ttacaaggaa tgcagtgttt gtgaccgtcg 60
gtgcctttgc taaggcagtg agtagtcttc tgaacaatac atcagtccac aatgcagaca 120
ctctacttcg cctagttcga tctcggccgc ctggtgtacc tctcatcact gttagcaatc 180
acatgtcaac gttagatgat cctctgatgt ggggattcaa gggattccca atcatgggat 240
gcgaaattgt ttcgatgggt atgggctgct gaagacatct gtttcaggaa ttcttttcat 300
tcttacttct ttcgcatggg gaaatgtatt cccattacaa gaggtggggg aatttatcgg 360
agccacatga atgaag 376

<210> 12
<211> 418
<212> DNA
<213> Linum usitatissimum

<220>
<221> misc_feature
<222> (1)..(418)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 12
ccgcctggtg tacctctcat cactgttagc aatcacatgt caacgttaga tgatcctctg 60
atgtggggat tcaagggatt cccaatcatg aatgcgaaat tgtttcgatg ggtattagct 120
gctgaagaca tctgtttcag gaattctttt cattcttact tctttcgcat ggggaaatgt 180
attcccatta caagaggtgg tggaatttat caaagccaca tgaatgaagc tcttcagcgc 240
ttgagcaatg gtgattggct gcacacattc cctgagggaa aggtcaacca agaaattgga 300
cctataagac gattgaaatg gggaactgcc agtctcatcg tccgtgcccc tgttacaccg 360
atagtattac ccattgttca tcgtggcttt caagaggtga tgccagagaa ctacctat 418

<210> 13
<211> 445
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(445)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 13
ttccgggtcg accgccattg gcgccgccgc cactaccacc acacctttat cccctccgcc 60
gatggctact tctcctccac cattcaacgc tggctcagcc gatttcgtga tttccgcaga 120
gactcgttgc cgtcgtccac ctcttttttat cgcaaacgag tgattaagga tttcagttct 180
gaagaagatt caactcttgt tcgtatgatg caagctgttg cggttcctgt tcttggaaat 240
gtctgtcacg tgtttatgaa cggattaaac agtgtgcagg tatatggttt agaaaaactg 300
cactccgctt tactgcaaag acctaaagga aaacctcttc ttacggtcag caatcatgtt 360
gcttccatgg atgatcctct tgttattgct tcgctgcttc ctccgagtgt tcttttggac 420
gctaggaatc tcagatggac gcttc 445

<210> 14
<211> 361
<212> DNA
<213> Hordeum vulgare

<220>
<221> misc_feature
<222> (1)..(361)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 14
ggaatcggtg atcctccgca tggttcaagc tgtggcggtt cctctattgg gaaacatgtg 60
ctacgtgttc atgaatggcc tcaatcgcgt tcaggttcat ggcctggaga agctgcacaa 120
ggcattgctt gagaggccta aggacaagcc cctagtaacg gttagcaacc atgttgcttc 180
tgtcgatgac ccatttgtga ttgcttcatt gctaccacca agagtacttt tggatgctca 240
gaacttgagg tggacacttt gcgcaacgat cgctgtttta ggaatcccgt cacttctgca 300
ttctttaaga ctgtcaaagt cttgcccctc tctcgtggtc atggagttta tcagaagggt 360
a 361

<210> 15
<211> 472
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(472)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 15
tgtatcggaa tttccgggtc gacgaccacc gccggagagc cgcggtttta tatacggacg 60
gttacttctc ttcctccatc caccgcttgg ctgctcgatt gcggaacttc cgccgcgagt 120
ctctcccttc tgcccccgct ttttatcgca gaagagtacc taaagatttg acggcagaag 180
aagagtctgc tatcttccgg atgcttcaag ctgtggctgt tccacttatt ggaaacgctt 240
gtcatgtttt catgaatggt cttaaccgtg ttcaggtgta tggtttagag aagttgcatg 300
atgctctgct caacaggcca aagaacaagc ctctcgtaac ggttagcaat catgtggcat 360
ccttggatga tccatttgtc attgcttcgt tacttccgcc taagcttcta ctcgatgctc 420
gtaatttgag gtggacgctt tgtgctacag atagatgctt taagaaccct gt 472

<210> 16
<211> 412
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (412)..(412)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(412)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 16
tttagatgat ccagtaatgt ggggagggtt caaggcgtct tctttcctta gatccagagc 60
tggctcgatg ggttcttgct gcagaggaca tttgtttcaa gaaccctgtc ttctcctaca 120
tcttccgcac tggcaagtgt atacctataa ctagaggtgg tggaatctac caagaacaca 180
tgagtgaagc tctcgagcga ttaaaagatg gatcttggtt gcataccttc ccagagggca 240
aggtgtttca agaagatgtg cctataagac gacttaaatg gggaaccgca agcctcatcg 300
cccgttgccc agtcacccca atcgtcttgc caataattca ccgtggtttg acgagatgaa 360
tgccgagagt acatttatgg aaaangacca ccgtacccgt tgggaacaaa an 412

<210> 17
<211> 410
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (410)..(410)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(410)

<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 17
tttagatgat ccagtaatgt ggggagggtt caagggtctt ctttccttag atccagagct 60
ggctcgatgg gttcttgctg cagaggacat ttgtttcaag aaccctgtct tctcctacat 120
cttccgcact ggcaagtgta tacctataac tagaggtggt ggaatctacc aagaacacat 180
gagtgaagct ctcgagcgat taaaagatgg atcttggttg cataccttcc cagagggcaa 240
ggtgtttcaa gaagatgtgc ctataagacg acttaaatgg ggaaccgcaa gcctcatcgc 300
ccgttgccca gtcacccaaa tcgtcttgcc aatatttcac cgtggttttg acaacatgat 360
gcccgaaaat gtccttttat ggaagaatga caaccgtacc tgtggggaan 410

<210> 18
<211> 420
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (420)..(420)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(420)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 18
gccattggcg ccgccgacac aaccaccaca cctttatccc ctccgccgat ggctacttct 60
cctccaccat tcaacgctgg ctcagccgat ttcgtgattt ccgcagagac tcgttgccgt 120
cgtccacctc tttttatcgc atacgagtga ttaaggattt cagttctgaa gaagattcaa 180
ctcttgttcg tatgatgcaa gctgttgcgg ttcctgttct tggaaatgtc tgtcacgtgt 240
ttatgaacgg attaaacagt gtgcaggtat atggtttaaa aaaactgcac tccgctttac 300
tgcaaagacc taaaggaaaa cctcttctta cggtcagcaa tcatgttgct tccatggatg 360
atcctcttgt tattgcttcg ctgcttcctc cgagtgttct tttggacgct aggaatctcn 420

<210> 19
<211> 490
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (397)..(397)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(490)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 19
aattcctggg tcgacgattt cgtcccgaga tggtggcaag actatgggct cagcaaaaag 60

aggtattgga aggttgattt tggacgcaga taccctccct atggttgttc catttgtgca 120
tactggtatg caagatataa tgcctatagg agccagtgtt ccacggattg gcaaaacagt 180
gacagtgatc attggagatc ctattccctt taatgacctt gtagacactg aaggagccaa 240
acacgtttca aggaagcagt tgtatgacgc tgtatcttcc aggataggac aaagattaca 300
ccagttaaag caacaggttg ataaagtatc tctgggagca caatattcag aagaatcacc 360
agcccttctt ggtaaacaaa tttcccaaac cgatgtncgt ctcaatggtt tggactggca 420
tgttcctaaa agggattgcc atccgaagga agcatcagcc tgaaggttaa gaggtttatg 480
gactctacag 490

<210> 20
<211> 386
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)..(386)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 20
cgtgcttaga aatggaggct ggctgcatac attccctgaa ggaaaaatag cccaagaaga 60
tcagccgatt agaagattga agtggggaac ggccagtctt attgtccgag cacctataac 120
tccaatagtt ttgccaattg ttcactctgg tttcgaaaag gtcatgccag aaaactcgtt 180
ctttggacgg cgaccaccgg tgccactctg cagtaagaag atagacatca ttgttggaga 240
gccaatagag tttgacttgc caagcttgaa gcaagaagca tcaacggtac cccatgactc 300
atcctctgaa cggaaggggt ggccggccat tacaccagat gggctggacg aggccgccca 360
gagatggctt taccagaaga tgtcag 386

<210> 21
<211> 429
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(429)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 21
ctcgggtcga cgattccgta cggtcttaac cgagttcagg tgtatggttt atagaagctg 60
tatgatgctc tgctcaacag gccaaagaac aagcctctcg taacggctaa caatgatgtg 120
gcatccttgg atgatccatt cgccattgct tcattactat ccgcctaagc ttctactctg 180
atgctcgtaa tttgaggtgg acgctttgtg ctacagatag atgctttaag aaccctgtaa 240
cttcagcttt ctttcgatca ttcaaagttt tgccagcttc tcgcggtgaa ggaatctatc 300
agcagggaat ggacatcgcg acgtcgaaat tgaataatgg aggatgggtt cacatatttc 360
cagaaggcag acggtaccga gatggtggct agactatggg ttcacgcaat agaggtattg 420
gaatgttgt 429

<210> 22
<211> 436
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(436)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 22
tctagatgac ccactattgt ggggagggct ccagggtctt atttccttag atccaaagct 60
ggctcgatgg gatcttgctg cagaggacat ttgtttcaat aaccctgtct tctcctacat 120
tttccgcact gacacgcgta tacctataac tagaggtggt ggaatctacc aagaacacat 180
gagtgaagct ctagagcgat taatagatgg atcttgcacg gcaaggcgtt tcaagaagat 240
gtgcctataa gacgacttaa atggggaacc gcaagcctca tcagccgttg cccagtcacc 300
ccaatcgtct tgccaataat tcaccgtggt tctgacgaga tgatgccgga gaagtacatt 360
tatggaagaa taccaccgtt accgctgtgg aacaaaaacc ttaaagtagt tgttggtgaa 420
ccaatcagag ttgatg 436

<210> 23
<211> 423
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (423)..(423)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(423)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 23
ggatgatcca tttgtcattg cttcgttact tccgcctaag cttctactcg atgctcgtaa 60
tttgaggtgg acgctttgtg ctacagatag atgcttcaaa aaccctgtaa cttcagcttt 120
ctttcgatcc gtcaaggttt tgccagtttc tcgcggtgaa ggaatttatc agcagggaat 180
ggacattgcg atttcgaaat tgaataatgg aggatgggtt cacatatttc cagaaggtag 240
tcgctcccga gatggtggca agactatggg ctcagcaaaa agaggtattg gaaggttgat 300
tttggacgca gataccctcc ctaatgttgt tccatttgtg catactggta tgcaagatat 360
aatgcctata ggagccagtg ttccacggat tggcaaaaca gtgacagtga tcattggaga 420
tcn 423

<210> 24
<211> 400
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(400)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 24

gcgatggcat ctaccaaaag ggaatggaca tggcactttc aaagttgaac aatggtggat 60
gggttcatat tttcccagaa ggaagtcgtt caaaggatgg agggaaaacc gtcgctcctg 120
ccaagagagg tgttggaaga ttggtaatgg acgctgacag ccttccagtt gtaataccct 180
ttgtccatac aggaatgcag gatataatgc ctgtcggaaa acgtattcca agagcaggca 240
aaagggtgat tgtggttgtt ggtgatccaa tcaacttcaa cgaccttatc attgacaaca 300
gcgatgaaac ccaacacatc tctagaggca ttttgtatga caaagcaaca gaaaggattg 360
ggcagagact gcaggaactg aaagccgaag tcgatagatt 400

<210> 25
<211> 414
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(414)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 25
ggcagcaaga tctgatcact tgggaggaat cccaagaaaa actgtgataa cagccgttgg 60
tgctttcgcg agagcagtag ctaatctttg caacaaaacc aaagttcaca atgcagatac 120
tcttatgact cttgtccgtt cacgaccacc tggtgtccct ctcatcactt ttagatgatc 180
cagtaatgtg gggagggttc aagggtcttc tttctttaga tccagagttg gctcgatggg 240
tgcttgctgc tgaggatata tgtttcaaga actctttctt ctcctacatc ttccgcactg 300
gcaagtgtat acctataact agaggtggtg gaatctatca agaacacatg agtgaagctc 360
ttgaacgatt aaaagatgga tcttggttgc ataccttccc agaggggcag gtgg 414

<210> 26
<211> 397
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(397)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 26
ctgcccccgc tttttatcgc agaagagtac ctaaagattt gacggcagaa gaagagtctg 60
ctatcttccg gatgcttcaa gctgtggctg ttccacttat tggaaacgct tgtcatgttt 120
tcatgaatgg tcttaaccgt gttcaggtgt atggtttgga gaagttgcat gatgctttac 180
tcaacagacc aaagaacaag cctcttgtaa cggttagcaa tcatgtggcg tccttggatg 240
atccatttgt cattgcttcg ttacttcctc ctaagcttct acttgatgct cgtaatctga 300
ggtggacgct ttgtgctaca gatagatgct ttaagaaccc tgtaacttca gctttctttc 360
gatccgtcaa agttttgcca gtttctcgcg gtgaagg 397

<210> 27
<211> 429
<212> DNA
<213> Brassica napus

<220>

<221> misc_feature
<222> (1)..(429)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 27
gaattcaacg tcgacgattt cgtcgatccg tcaaggtttt gccagtttct cgcggtgaag 60
gaatttatca gcagggaatg gacattgcga tttcgaaatt gaataatgga ggatgggttc 120
acatatttcc agaaggtagt cgctcccgag atggtggcaa gactatgggc tcagcaaaaa 180
gaggtattgg aaggttgatt ttggacgcag ataccctccc tatggttgtt ccatttgtgc 240
atactggtat gcaacatata atgcctatag gagccactgt tccacggatt gacaaaacag 300
tgacagtgat cattggagat cctattccct ttagtgacct tgtagacact gaacgatcca 360
aacacgtttc aaggaaccag gtttatgacc ctctatcgtt caggatcgac agcgattacc 420
ctcctgcat 429

<210> 28
<211> 404
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(404)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 28
gttacttccg cctaagcttc tactcgatgc tcgtaatttg aggtggacgc tttgtgctac 60
agatagatgc ttcaaaaacc ctgtaacttc agctttcttt cgatccgtca aggttttgcc 120
agtttctcgc ggtgaaggaa tttatcagca gggaatggac attgcgattt cgaaattgaa 180
taatggagga tgggttcaca tatttccaga aggtagtcgc tcccgatatg gtggcaagac 240
tatgggctca gcaaaaagag gtattggaag gtgagtcata tatgccttta ctttcagcta 300
ctttatgtaa tgcgtgtgta tggaccttat tataacacaa acaagcttgt gattcacttc 360
tttgtgcaag atgatttctc tctcagatac catgcgtatg aatg 404

<210> 29
<211> 467
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (467)..(467)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(467)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 29
gaattctcgg gtcgacgata gtgcaaattt agatgatcca gtaatgtggg gagggttcaa 60
ggtcttcttt ccttagatcc agagctggct cgatgggtac ttgctgcaga ggacatttgt 120
ttcaagaacc ctgtcttctc ctacatcttc cgcactggca agtgtatacc tataactaga 180

ggtggtggaa tctaccaaga acacatgagt gaagctctcg agcgattaaa agatggatct 240
tggttgcata ccttcccaca gggcacggtg ttacacgatg atgtgcctag ctgacgactt 300
acatggggaa ccggcggcct aatcccgcgt tgaccaacca cgccaattct cttgccaata 360
tttcacggcg actgtgacga catcatgacg cagaaggcca tggatctata aacaccaccg 420
ctacctctct tgatcaaaac cgtaaacgta gaggaggcta accctcn 467

<210> 30
<211> 459
<212> DNA
<213> Brassica napus

<220>
<221> misc_difference
<222> (1)..(459)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 30
gatcaccgtg gtagagccgc ggttttatat acggcacggt atagcgttct cttctccatc 60
caccgcttgg ctgctcgatt ccggaacttc cgccgcgagt ctctcccttc tgcccccgct 120
ttttatcgca gaagagtacc taaagatttg acggcagaag aagagtctgc tatcttccgg 180
atgcttcaag ctgtggctgt tccacttatt ggaaacgctt gtcatgtttt catgaatggt 240
cttaaccgtg ttcaggtgta tggtttagag aagttgcatg atgctctgct caacaggcca 300
aagaacaagc ctctcgtaac ggttagcaat catgtggcat ccttggatga tccatttgtc 360
attgcttcgt tacttccgcc taagcttcta ctcgatgctc ggaatttgag gtggacgctt 420
tgggctacac acagatggtt taccaaccct gtgcttccg 459

<210> 31
<211> 389
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(389)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 31
ggggtactgc gcccgcaatt cccggnccgg accaccattg gcgccgcgac accaccacac 60
ctttatcccc tctgccgatg gctacttctc ctcgaccatt caacgctgcc tcagccgatt 120
tcgtgatttc cgaaggtatt cattgccttc ttccacctct ttctatcgta aacgagtgat 180
taaggatttc agttctgagg aagattcagc tcttgttcgg acgatgcaag ctgttgcggt 240
tcctgttctt ggaaatgtct gtcacgtgtt tatgaacgga ttaaaccagg tgcaggtgta 300
tggtttagaa aaactgcact ccgcgttgct gcatagacct aagggcaaac ctcttcttac 360
ggtcagcaat catgttgctt ccatggatg 389

<210> 32
<211> 400

<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(400)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 32
agaaaaactg cactccgctt tactgcaaag acctaaagga aaacctcttc ttacggtcag 60
caatcatgtt gcttccatgg atgatcctct tgttattgct tcgctgcttc ctccgagtgt 120
tcttttggac gctaggaatc tcagatggac gctttgcgca actgataggt gttttaaaaa 180
ccctgtgact tctgcattct ttcgatcagt caaagttttg ccagtttctc gaggtgatgg 240
catttatcaa gaaggaatgg acttggccat atcaaaattg aaccatggtg gttgggtcca 300
gatattccca cacggcggtt gatccctcta tttttcaaaa tcagaaagtt aaaataaggg 360
agggggcgtc gaaaaatcca agcggggagc gggccccttg 400

<210> 33
<211> 449
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (432)..(432)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(449)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 33
aattcccggg tcgacgatca ccgtggcaga gccgcggttt tatatacgga cggttacttc 60
tcctcctcca tccaccgctt ggctgctcga ttccggaact tccgccgcga gtctctccct 120
tctgcccccg ctttttatcg cagaagagta cctaaagatt tgacggcaga agaagagtct 180
gctatcttcc ggatgcttca agctgtggct gttccactta ttggaaacgc ttgtcatgtt 240
ttcatgaatg gtcttaaccg tgttcaggtg tatggtttgg agaagttgca tgatgcttta 300
ctcaacagac caaagaacaa gcctcttgta acggttagca atcatgtggc gtccttggat 360
gatccatttg tcattgcttc gttacttcct cctaagcttc tacttgatgc tcgtaatctg 420
aggtggacgc tntgtgctac agatagatg 449

<210> 34
<211> 429
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (216)..(216)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (1)..(429)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 34
ccgggatggt ggaaaaacca tgggctcttc caagagaggt gttgggaggt tagtcctgga 60
tggagatagc atgcctgttg ttgtcccatt tgtacataca gggatgcagg agattatgcc 120
tgtaggtgct aactttccca gaataggcaa gatggttaca gtgctcatag gtgatccgat 180
caatttttgat gatataattg aatttgacaa agacanaggc tcaaatgtgc ccagaagacg 240
actatatgat gcagtagcat ctaaaattgg tgatcggttg cttgagatga aggtccaggt 300
tgacactatc gcaattgtca agaaatgcag gtaccagaaa agtcctcaca cagactgacc 360
gaccattaaa aaactgagcc aggtgattgg gactaatttg aatggacatc ttctggccgc 420
agaaatgcc 429

<210> 35
<211> 449
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (432)..(432)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1)..(449)
<223> nucleic acid sequence which can be used to identify and clone genes encoding oil synthesis enhancing proteins (OEPs)

<400> 35
aattcccggg tcgacgatca ccgtggcaga gccgcggttt tatatacgga cggttacttc 60
tcctcctcca tccaccgctt ggctgctcga ttccggaact tccgccgcga gtctctccct 120
tctgcccccg ctttttatcg cagaagagta cctaaagatt tgacggcaga agaagagtct 180
gctatcttcc ggatgcttca agctgtggct gttccactta ttggaaacgc ttgtcatgtt 240
ttcatgaatg gtcttaaccg tgttcaggtg tatggtttgg agaagttgca tgatgcttta 300
ctcaacagac caaagaacaa gcctcttgta acggttagca atcatgtggc gtccttggat 360
gatccatttg tcattgcttc gttacttcct cctaagcttc tacttgatgc tcgtaatctg 420
aggtggacgc tntgtgctac agatagatg 449

<210> 36
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(23)
<223> 5' primer for the YPR140w gene

<400> 36
atgtctttta gggatgtcct aga 23

<210> 37
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(23)
<223> 3' primer for the YPR140w gene

<400> 37
tcaatcatcc ttacccttg gtt 23

<210> 38
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(21)
<223> primer At140.1-S1

<400> 38
gtcggtcttt ctaactgaat c 21

<210> 39
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer At140.1-A1

<400> 39
cctgtgggac ttaaacctca 20

<210> 40
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer At140.1-S2

<400> 40
cagaatggga attcattttg 20

<210> 41

<211> 21
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(21)
<223> primer At140.1-A2

<400> 41
ctaacgggag tttaacttgc a 21

<210> 42
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(19)
<223> primer At140.2-S1

<400> 42
ctggtctcgt ttctaattg 19

<210> 43
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> (1)..(22)
<223> primer At140.2-A1

<400> 43
catggcgaat ctaaaccgga ac 22